



COPY

1/6

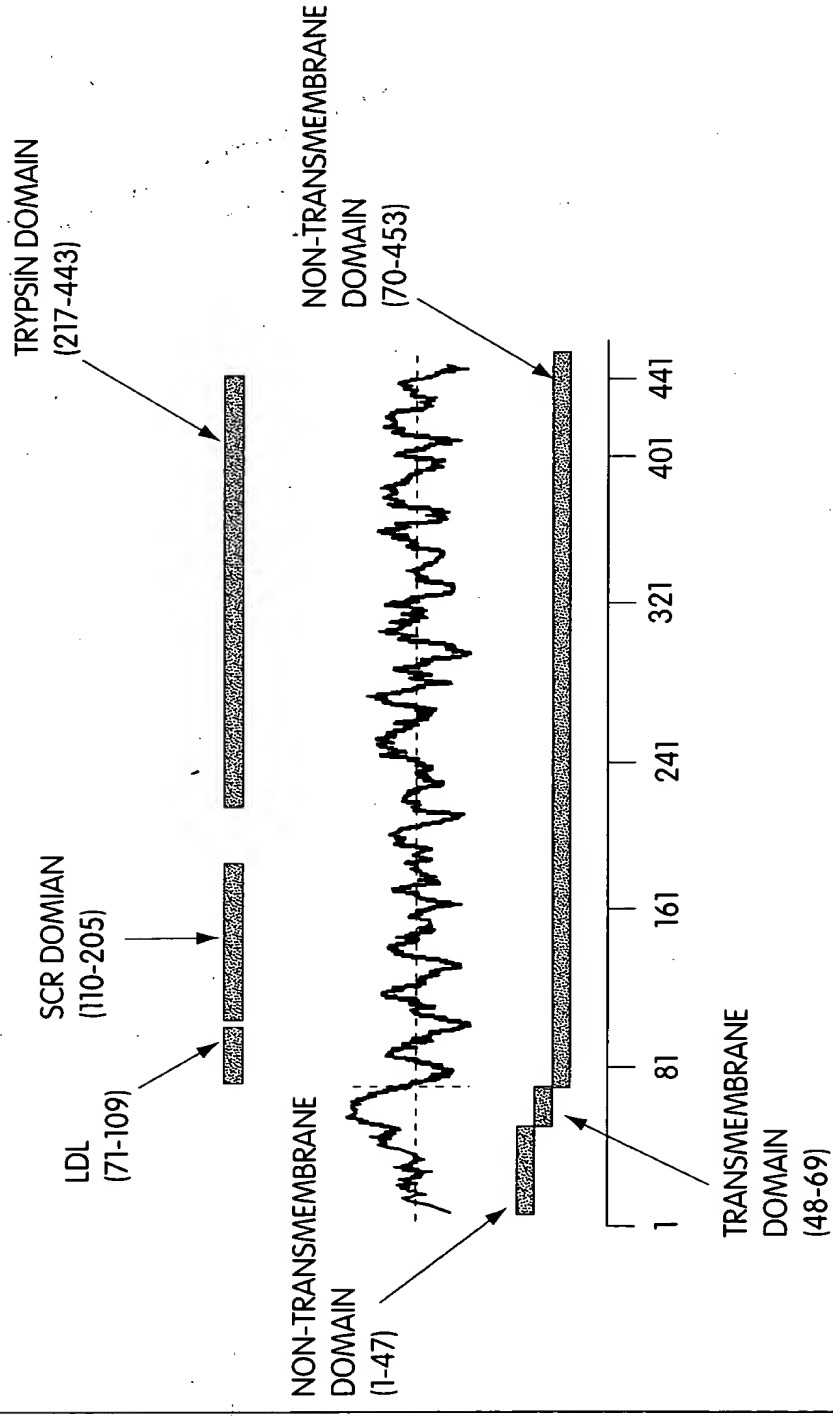


Fig. 1



2/6

trypsin: domain 1 of 1, from 217 to 443: score 293.0, E = 3.2e-92  
\*->IvGGreaqpgsfsgsPwqvslqvrsgggsrkhfCGGSLisenwVLTAA  
IvGG + ++ Pwq+slq+ + +h+CGGS+i + w++TAA  
14094 217 IVGGNMSLLSQW--PWQASLQFQG-----YHLCGGSVITPLWIITAA 256  
  
HCvsgaasapassvrVSlsvrlGehnlsltegteqkfdvkktiivHpnyn  
HCv++ +++s+++ +G +sl + v+k i+ H++y  
14094 257 HCVYD--LYLPKSWTI----QVGL--VSLLDNPAPSHLVEK-IVYHSKYK 297  
  
pdtldngaYdnDiAlLkLkspgvtlgdtrpicLpsassdlpvGttctvs  
p+ l+ nDiAl+kL++p +t+++ ++p+cLp + ++p+G c+ s  
14094 298 PKRLG-----NDIALMKLAGP-LTFNEMIQPVCLPNSEENFPDGKVCWTS 341  
  
GwGrrptknlgl.sdtLqevvvpvvsretCrsayeyggtDkvefvtdnm  
GwG t+++g+ s +L ++ vp++s++ C+++ ygg +++ m  
14094 342 GWGA--TEDGGdASPVLNHAAPLISNKICNHRDVYGGI-----ISPSM 383  
  
iCagal.ggkdaCqGDSGGPLvcsgdnrdgrwlvGivSwGsygCargnk  
+Cag+l+gg+d+CqGDSGGPLvc w+lvG +S+G gCa+ nk  
14094 384 LCAGYLtGGVDSCQGDSSGGLVCQER---RLWKLVGATSFG-IGCAEVNK 429  
  
PGvytrVssyldWI<-\*  
PGvytrV+sldWI  
14094 430 PGVYTRVTSFLDWI 443

Fig. 2A

trypsin\_2: domain 1 of 1, from 216 to 443: score 328.2, E = 9.2e-95  
\*->RIVGGseakigsfPwqvslq.....CGGSLisprwVLTAAHC....  
RIVGG+ + ++Pwq+sLq ++ + CGGS+I+p w++TAAHC +  
14094 216 RIVGGNMSLLSQWPWQASLQfgyhlCGGSVITPLWIITAAHCvydl 262  
  
.....rVrlGshdlssgeeteggprldspggqvikVskiievHpnYn..  
+++ ++ +G +l + + + V+ki+ H +Y ++  
14094 263 ylpkswTIQVGLVSLLDNP-----APSHLVEKIV-YHSKYKpk 299  
  
...NDIALLkLkeptlstdsntvrPicLPssneiktsegntvpaGttctV  
+ +NDIAL+kL+ p+t+++ ++P+cLP+s +++p+G c+  
14094 300 rlgNDIALMKLAGPLTFNE--MIQPVCLPNS-----EENFPDGKVCWT 340  
  
sGWGrtsegpeesggslpdvLqevnvpivsnetCr.....Ml  
sGWG t++ gg + vL ++ vp++sn+ C+++ +++ ++Ml  
14094 341 SGWGATED-----GGDASPVLNHAAPLISNKICNhrdvgygiispsML 384  
  
CAGyleggntpgGkDaCqGDSGGPLvc.....vLvGiVSWGsssslygCa  
CAGyl+ gG+D+CqGDSGGPLvc+++ ++LvG +S+G +gCa  
14094 385 CAGYLT-----GGVDSCQGDSSGGLVCqerrlwKLVGATSFG---IGCA 425  
  
rpnkPGVYTrVssyldWI<-\*  
+ nkPGVYTrV+sldWI  
14094 426 EVNKPVG YTRVTSFLDWI 443

Fig. 2B



3/6

BEGIN SEQ ID NO: 6      END SEQ ID NO: 6

\*->stCggpdeFqCgsgrrCIprswvCDGdpDCeDGSDEslenCaa<-\*

+C+ +++C+s+ CI +CDG DC+DG+DE +C++

14094 71 FDCS--GKYRCRSSFKCIELIARCDGVSDCKDGEDE--YRCVR 109

Fig. 3A

BEGIN SEQ ID NO: 7

\*->vgGssrCeGrVEVrhdgskWgtVCdssWslrdanvdpQaskvCrqLG

vgG +++ ++V+ + W+t C+++W + anv +C+qLG

14094 110 VGG--QNA-VLQVF-TAASWKTMCSDDWKGHYANV-----ACAQLG 146

CGgavsl1.gpyfsegggPagqreiwldgvnCsGnE...tsLsqCpvrvt

+ vs+ + s+ g +++++ + +++ +

14094 147 FPSYVSSDnLRVSSLEG-----QFREEFVSIDHLLpdDKVTALHHS-- 187

ppglrqrqshdgedagVvCs<-\*

++ ++c g+ + ++C

14094 188 -VYVREGCAS-GHVVTLQCT 205      END SEQ ID NO: 7

Fig. 3B



4/6

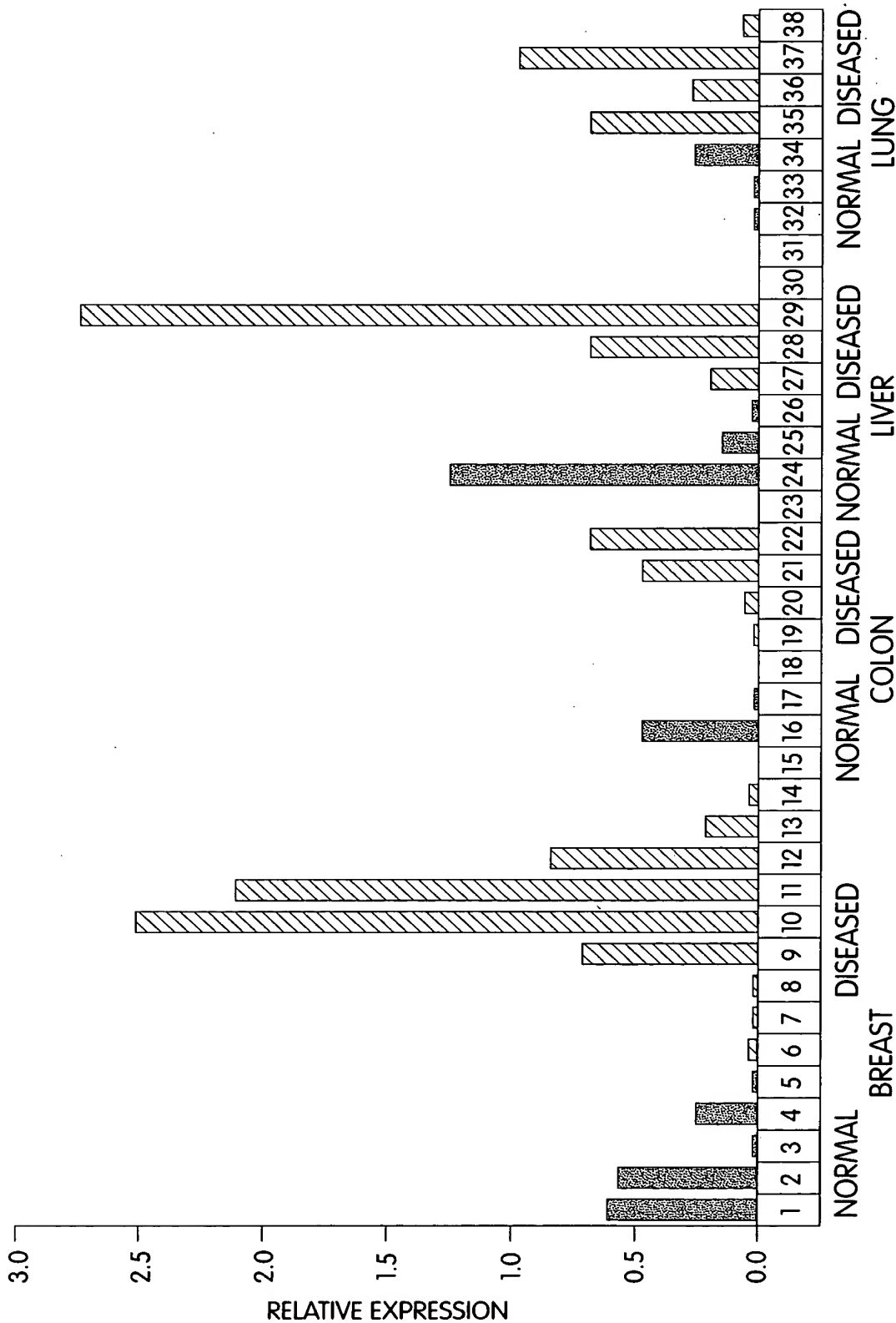


Fig. 4



5/6

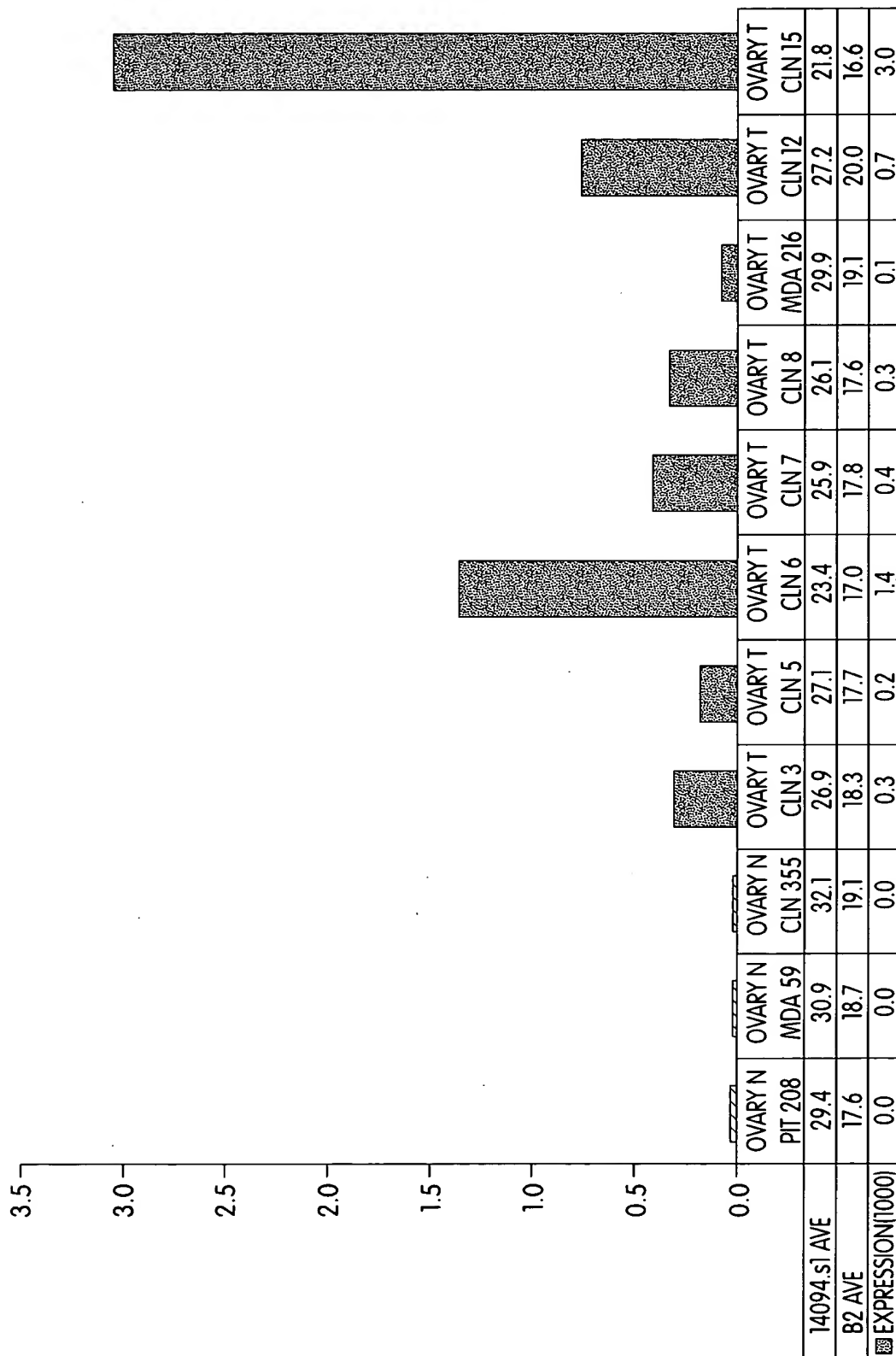


Fig. 5



6/6

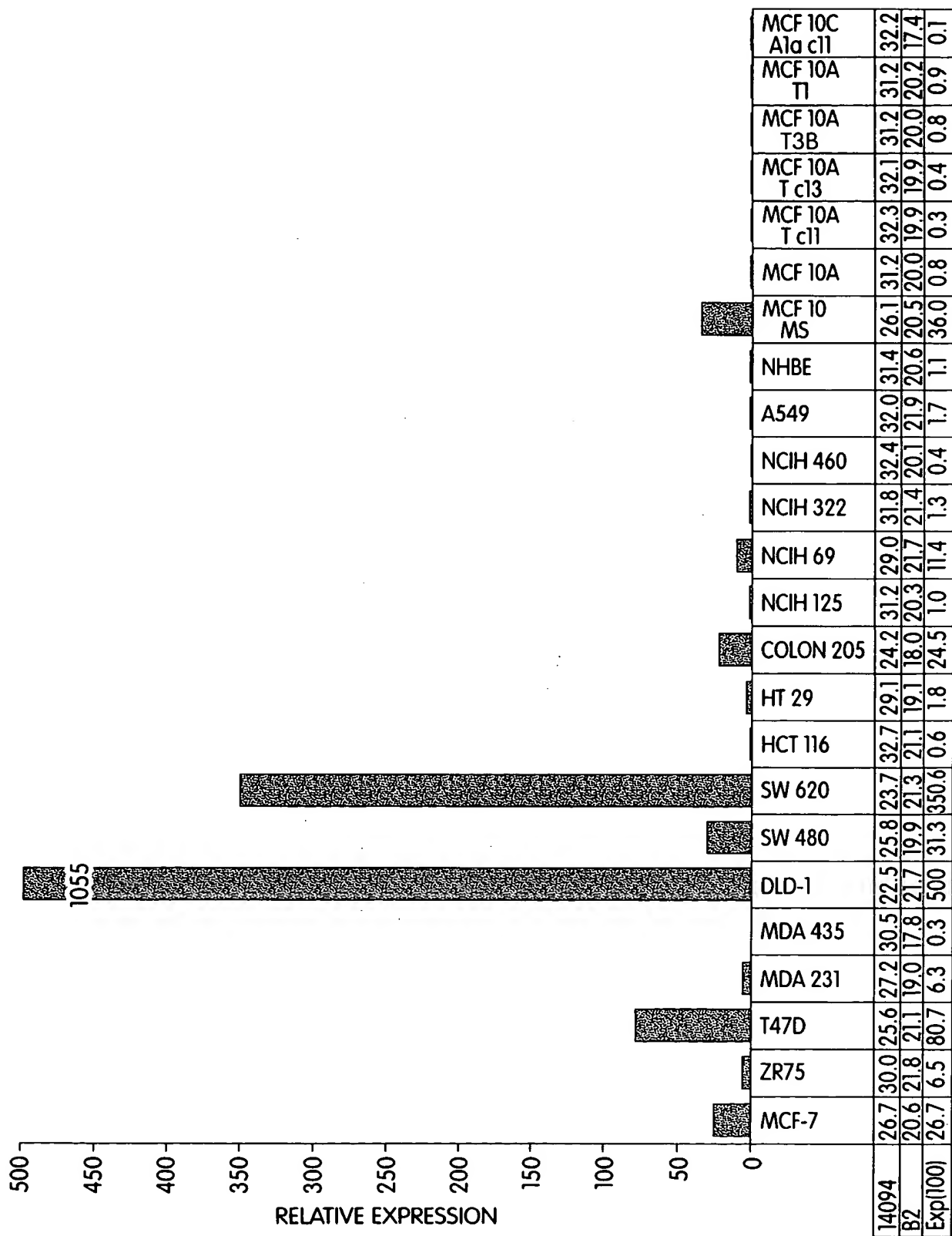


Fig. 6